

The Developmental Transcriptome of the Mosquito *Aedes aegypti*, an invasive species and major arbovirus vector.

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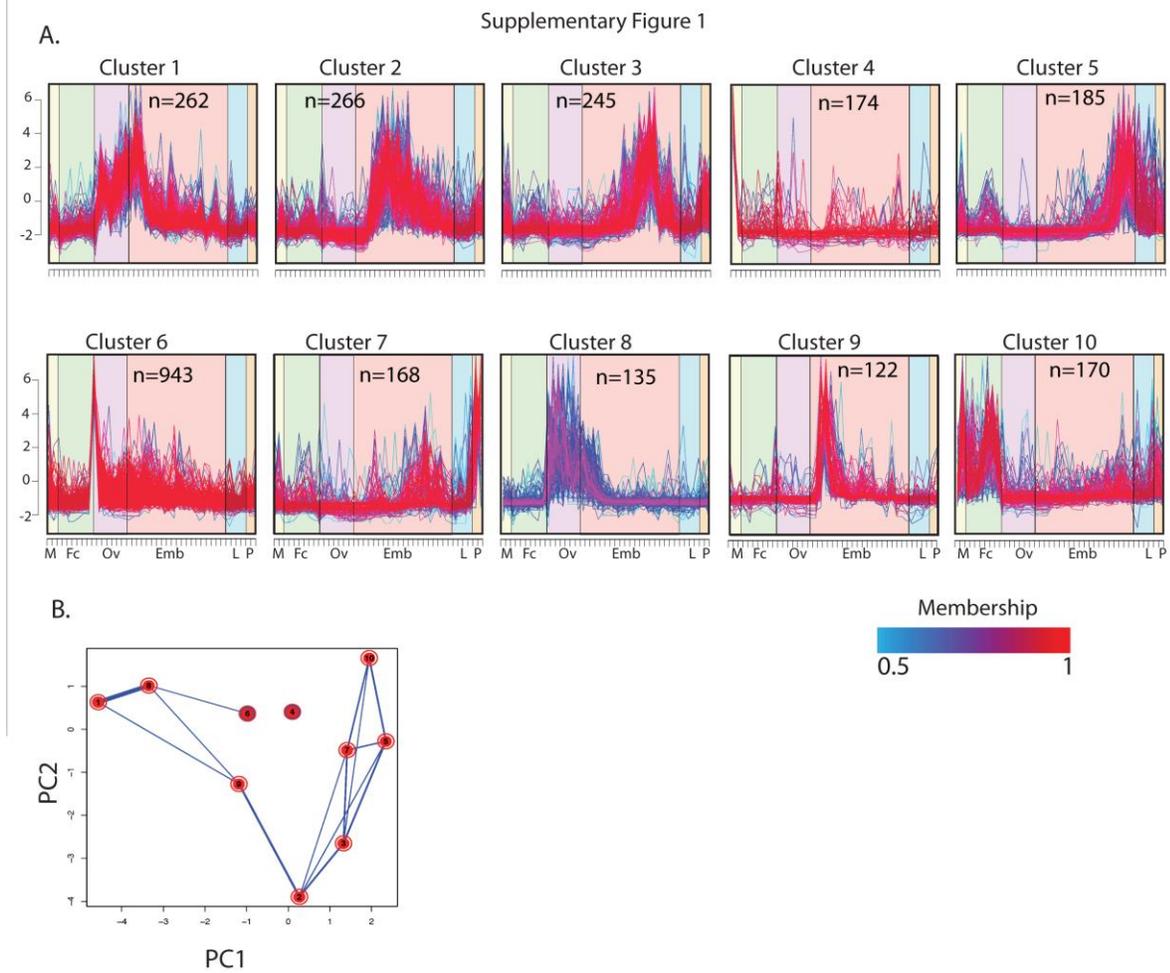


Figure S1 Soft Clustering of NTRs. 10 NTR expression profile clusters are identified through soft clustering procedure. Each NTR is assigned a line color corresponding to its membership value, with red (1) indicating high association. The major developmental groups are organized as in Figure 1B-D (A). Principal component analysis shows relationships between the 20 clusters, with thickness of the blue lines between any two clusters reflecting the fraction of genes that are shared (B, thickness of blue lines). n= the number of genes in each cluster.

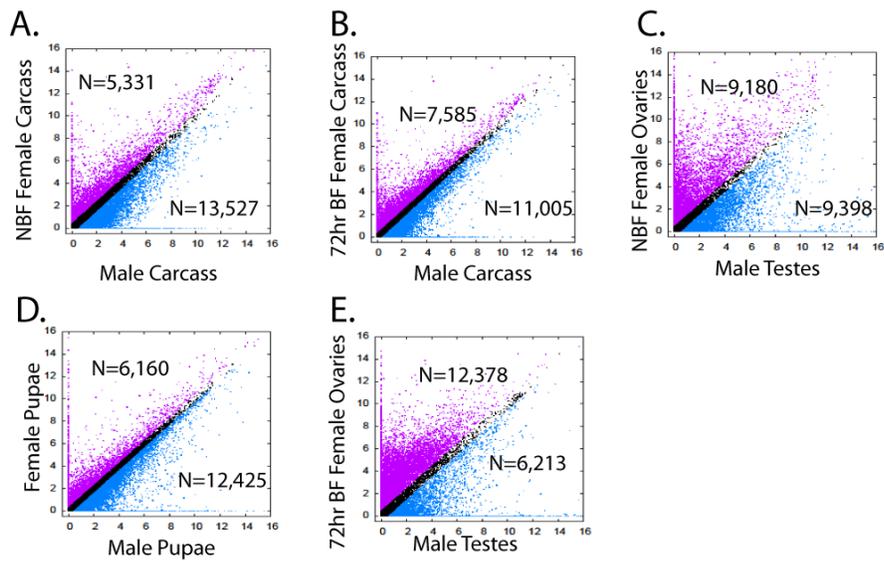


Figure S2 Scatter plots showing sex-biased gene expression. Scatter plots showing sex-bias in \log_2 for AAEL genes and NTRs. 50% of the data is unbiased (black). Male biased gene expression is indicated in blue, with points falling on the X-axis showing male-specific expression. Female biased gene expression is indicated in purple, with points falling on the Y-axis showing female-specific expression. N indicates the number of genes in each category. The comparisons include non blood-fed female carcass vs. male carcass (A), female carcass 72hrs post blood feed vs. male carcass (B), non blood fed ovaries vs. testes & AG (C), female pupae vs. male pupae (D), and 72hr PBM ovaries vs. testes & AG (E). Lists of male and female sex specific genes can be located in the supplement (supplementary tables 24, 25).

Files S1-S4
Supporting Files

Available for download as compressed files at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.006742/-/DC1>.

File S1. New Isoforms of Annotated genes GTF. A gene transfer format (GTF) file for the new isoforms of annotated genes.

File S2. NTR GTF.

A GTF file for all the NTRs.

File S3. Aggregated AAEL loci. A GTF file for the annotated AAEL genes which aggregate into loci.

File S4. Non-coding NTRs GTF. A GTF file for all the predicted non-coding NTRs.

Tables S1-S30
Supporting Tables

Available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.006742/-/DC1>.

Table S1. Summary of Sequenced Experimental Datasets. Summary of samples sequenced and type of sequencing performed: short poly(A+), paired-end poly(A+), small-RNA.

Table S2. Poly(A+) multi-map read and mapping statistics. Mapping statistics including percentages for each poly (A+) sample indicating the total reads produced, total reads mapped to junctions, total reads mapped to exons, total reads mapped uniquely, total reads mapped to multiple locations, and total reads mapped.

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